OIPE

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/839,136

DATE: 11/08/2001
TIME: 12:15:49

Input Set : **A:\2356-7 Sequence Listing.txt**
Output Set: **N:\CRF3\11082001\I839136.raw**

```
 4 <110> APPLICANT: Naoyuki TANIGUCHI et al.
 6 <120> TITLE OF INVENTION: ALPHA 1-6 FUCOSYLTRANSFERASE
 9 <130> FILE REFERENCE: 2356-7
11 <140> CURRENT APPLICATION NUMBER: 09/839,136
12 <141> CURRENT FILING DATE: 2001-04-23
14 <150> PRIOR APPLICATION NUMBER: 09/442,629
15 <151> PRIOR FILING DATE: 1999-11-18
17 <150> PRIOR APPLICATION NUMBER: 08/913,805
18 <151> PRIOR FILING DATE: 1998-01-07
20 <150> PRIOR APPLICATION NUMBER: PCT/JP97/00171
21 <151> PRIOR FILING DATE: 1997-01-23
23 <160> NUMBER OF SEQ ID NOS: 15
25 <170> SOFTWARE: FastSEQ for Windows Version 4.0
27 <210> SEQ ID NO: 1
28 <211> LENGTH: 1728
29 <212> TYPE: DNA
30 <213> ORGANISM: Pig
32 <220> FEATURE:
33 <221> NAME/KEY: CDS
34 <222> LOCATION: (1)...(1728)
36 <400> SEQUENCE: 1
37 atg cgg cca tgg act ggt tcg tgg cgt tgg att atg ctc att ctt ttt    48
38 Met Arg Pro Trp Thr Gly Ser Trp Arg Trp Ile Met Leu Ile Leu Phe
39 1               5                   10                  15
41 gcc tgg ggg acc ttg cta ttt tac ata ggt ggt cac ttg gta cga gat    96
42 Ala Trp Gly Thr Leu Leu Phe Tyr Ile Gly Gly His Leu Val Arg Asp
43              20                  25                  30
45 aat gac cac tct gat cac tct agc cga gaa ctg tcc aag att ttg gca   144
46 Asn Asp His Ser Asp His Ser Ser Arg Glu Leu Ser Lys Ile Leu Ala
47          35                  40                  45
49 aag ctg gaa cgc tta aaa caa caa aat gaa gac ttg agg aga atg gct   192
50 Lys Leu Glu Arg Leu Lys Gln Gln Asn Glu Asp Leu Arg Arg Met Ala
51      50                  55                      60
53 gga tct ctc cga ata cca gaa ggc ccc att gat cag ggg cca gct tca   240
54 Gly Ser Leu Arg Ile Pro Glu Gly Pro Ile Asp Gln Gly Pro Ala Ser
55  65                  70                  75                  80
57 gga aga gtt cgt gct tta gaa gag caa ttt atg aag gcc aaa gaa cag   288
58 Gly Arg Val Arg Ala Leu Glu Glu Gln Phe Met Lys Ala Lys Glu Gln
59                  85                  90                  95
61 att gaa aat tat aag aaa caa act aaa aat ggt cca ggg aag gat cat   336
62 Ile Glu Asn Tyr Lys Lys Gln Thr Lys Asn Gly Pro Gly Lys Asp His
63              100                 105                 110
65 gaa atc cta agg agg agg att gaa aat gga gct aaa gag ctc tgg ttt   384
66 Glu Ile Leu Arg Arg Arg Ile Glu Asn Gly Ala Lys Glu Leu Trp Phe
67              115                 120                 125
69 ttt cta caa agt gag ttg aag aaa tta aag aat tta gaa gga aat gaa   432
70 Phe Leu Gln Ser Glu Leu Lys Lys Leu Lys Asn Leu Glu Gly Asn Glu
```

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```
71      130                    135                  140
73 ctc caa aga cat gca gat gaa ttt cta tca gat ttg gga cat cat gaa    480
74 Leu Gln Arg His Ala Asp Glu Phe Leu Ser Asp Leu Gly His His Glu
75 145                    150                  155                160
77 agg tct ata atg acg gat cta tac tac ctc agt caa aca gat ggg gca    528
78 Arg Ser Ile Met Thr Asp Leu Tyr Tyr Leu Ser Gln Thr Asp Gly Ala
79                     165                  170                  175
81 ggt gat tgg cgt gaa aag gag gcc aaa gat ctg aca gag ctg gtc cag    576
82 Gly Asp Trp Arg Glu Lys Glu Ala Lys Asp Leu Thr Glu Leu Val Gln
83                     180                  185                  190
85 cgg aga ata aca tat ctt cag aat ccc aag gac tgc agc aaa gcc aag    624
86 Arg Arg Ile Thr Tyr Leu Gln Asn Pro Lys Asp Cys Ser Lys Ala Lys
87           195                    200                  205
89 aag cta gtg tgt aat atc aac aaa ggc tgt ggc tat ggc tgt cag ctc    672
90 Lys Leu Val Cys Asn Ile Asn Lys Gly Cys Gly Tyr Gly Cys Gln Leu
91     210                    215                  220
93 cat cat gta gtg tac tgc ttt atg att gca tat ggc acc cag cga aca    720
94 His His Val Val Tyr Cys Phe Met Ile Ala Tyr Gly Thr Gln Arg Thr
95 225                    230                  235                240
97 ctc gcc ttg gaa tct cac aat tgg cgc tac gct act ggg gga tgg gaa    768
98 Leu Ala Leu Glu Ser His Asn Trp Arg Tyr Ala Thr Gly Gly Trp Glu
99                     245                  250                  255
101 act gtg ttt aga cct gta agt gag acg tgc aca gac aga tct ggc agc   816
102 Thr Val Phe Arg Pro Val Ser Glu Thr Cys Thr Asp Arg Ser Gly Ser
103           260                    265                  270
105 tcc act gga cat tgg tca ggt gaa gta aag gac aaa aat gtt cag gtg   864
106 Ser Thr Gly His Trp Ser Gly Glu Val Lys Asp Lys Asn Val Gln Val
107           275                    280                  285
109 gtt gag ctc ccc att gta gac agt gtt cat cct cgt cct cca tat tta   912
110 Val Glu Leu Pro Ile Val Asp Ser Val His Pro Arg Pro Pro Tyr Leu
111           290                    295                  300
113 ccc ctg gct gtc cca gaa gac ctt gca gat cga ctt gta cga gtc cat   960
114 Pro Leu Ala Val Pro Glu Asp Leu Ala Asp Arg Leu Val Arg Val His
115 305                    310                  315                320
117 ggt gat cct gca gtg tgg tgg gta tcc cag ttt gtc aag tac ttg att  1008
118 Gly Asp Pro Ala Val Trp Trp Val Ser Gln Phe Val Lys Tyr Leu Ile
119           325                    330                  335
121 cgc cca caa ccc tgg ctg gaa aag gaa ata gaa gag gcc acc aag aag  1056
122 Arg Pro Gln Pro Trp Leu Glu Lys Glu Ile Glu Glu Ala Thr Lys Lys
123           340                    345                  350
125 cta ggc ttc aaa cat cca gtt att gga gtc cat gtt aga cgc aca gac  1104
126 Leu Gly Phe Lys His Pro Val Ile Gly Val His Val Arg Arg Thr Asp
127           355                    360                  365
129 aaa gtg gga gcg gaa gca gcc ttc cat ccc att gag gaa tac acg gtg  1152
130 Lys Val Gly Ala Glu Ala Ala Phe His Pro Ile Glu Glu Tyr Thr Val
131     370                    375                  380
133 cac gtt gaa gaa gac ttt cag ctt ctt gct cgc aga atg caa gtg gat  1200
134 His Val Glu Glu Asp Phe Gln Leu Leu Ala Arg Arg Met Gln Val Asp
135 385                    390                  395                400
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137 aaa aaa agg gtg tat ttg gcc aca gat gac cct gct ttg tta aaa gag   1248
138 Lys Lys Arg Val Tyr Leu Ala Thr Asp Asp Pro Ala Leu Leu Lys Glu
139             405                 410                 415
141 gca aaa aca aag tac ccc agt tat gaa ttt att agt gat aac tct atc   1296
142 Ala Lys Thr Lys Tyr Pro Ser Tyr Glu Phe Ile Ser Asp Asn Ser Ile
143             420                 425                 430
145 tct tgg tca gct gga cta cat aat cga tat aca gaa aat tca ctt cgg   1344
146 Ser Trp Ser Ala Gly Leu His Asn Arg Tyr Thr Glu Asn Ser Leu Arg
147             435                 440                 445
149 ggt gtg atc ctg gat ata cac ttt ctc tcc cag gca gac ttc cta gtg   1392
150 Gly Val Ile Leu Asp Ile His Phe Leu Ser Gln Ala Asp Phe Leu Val
151     450                 455                 460
153 tgt act ttt tca tcg cag gtc tgt aga gtt gct tat gaa atc atg caa   1440
154 Cys Thr Phe Ser Ser Gln Val Cys Arg Val Ala Tyr Glu Ile Met Gln
155 465                 470                 475                 480
157 gcg ctg cat cct gat gcc tct gcg aac ttc cgt tct ttg gat gac atc   1488
158 Ala Leu His Pro Asp Ala Ser Ala Asn Phe Arg Ser Leu Asp Asp Ile
159             485                 490                 495
161 tac tat ttt gga ggc cca aat gcc cac aac caa att gcc att tat cct   1536
162 Tyr Tyr Phe Gly Gly Pro Asn Ala His Asn Gln Ile Ala Ile Tyr Pro
163             500                 505                 510
165 cac caa cct cga act gaa gga gaa atc ccc atg gaa cct gga gat att   1584
166 His Gln Pro Arg Thr Glu Gly Glu Ile Pro Met Glu Pro Gly Asp Ile
167             515                 520                 525
169 att ggt gtg gct gga aat cac tgg gat ggc tat cct aaa ggt gtt aac   1632
170 Ile Gly Val Ala Gly Asn His Trp Asp Gly Tyr Pro Lys Gly Val Asn
171     530                 535                 540
173 aga aaa ctg gga agg acg ggc cta tat ccc tcc tac aaa gtt cga gag   1680
174 Arg Lys Leu Gly Arg Thr Gly Leu Tyr Pro Ser Tyr Lys Val Arg Glu
175 545                 550                 555                 560
177 aag ata gaa aca gtc aag tac ccc aca tat ccc gag gct gac aag taa   1728
178 Lys Ile Glu Thr Val Lys Tyr Pro Thr Tyr Pro Glu Ala Asp Lys   *
179             565                 570                 575
183 <210> SEQ ID NO: 2
184 <211> LENGTH: 575
185 <212> TYPE: PRT
186 <213> ORGANISM: Pig
188 <400> SEQUENCE: 2
189 Met Arg Pro Trp Thr Gly Ser Trp Arg Trp Ile Met Leu Ile Leu Phe
190   1               5                  10                  15
191 Ala Trp Gly Thr Leu Leu Phe Tyr Ile Gly Gly His Leu Val Arg Asp
192             20                  25                  30
193 Asn Asp His Ser Asp His Ser Ser Arg Glu Leu Ser Lys Ile Leu Ala
194             35                  40                  45
195 Lys Leu Glu Arg Leu Lys Gln Gln Asn Glu Asp Leu Arg Arg Met Ala
196     50                  55                  60
197 Gly Ser Leu Arg Ile Pro Glu Gly Pro Ile Asp Gln Gly Pro Ala Ser
198 65                  70                  75                  80
199 Gly Arg Val Arg Ala Leu Glu Glu Gln Phe Met Lys Ala Lys Glu Gln
```

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```
200                     85                  90                  95
201 Ile Glu Asn Tyr Lys Lys Gln Thr Lys Asn Gly Pro Gly Lys Asp His
202                     100                 105                 110
203 Glu Ile Leu Arg Arg Arg Ile Glu Asn Gly Ala Lys Glu Leu Trp Phe
204             115                 120                 125
205 Phe Leu Gln Ser Glu Leu Lys Lys Leu Lys Asn Leu Glu Gly Asn Glu
206         130                 135                 140
207 Leu Gln Arg His Ala Asp Glu Phe Leu Ser Asp Leu Gly His His Glu
208 145                 150                 155                 160
209 Arg Ser Ile Met Thr Asp Leu Tyr Tyr Leu Ser Gln Thr Asp Gly Ala
210                 165                 170                 175
211 Gly Asp Trp Arg Glu Lys Glu Ala Lys Asp Leu Thr Glu Leu Val Gln
212             180                 185                 190
213 Arg Arg Ile Thr Tyr Leu Gln Asn Pro Lys Asp Cys Ser Lys Ala Lys
214         195                 200                 205
215 Lys Leu Val Cys Asn Ile Asn Lys Gly Cys Gly Tyr Gly Cys Gln Leu
216     210                 215                 220
217 His His Val Val Tyr Cys Phe Met Ile Ala Tyr Gly Thr Gln Arg Thr
218 225                 230                 235                 240
219 Leu Ala Leu Glu Ser His Asn Trp Arg Tyr Ala Thr Gly Gly Trp Glu
220             245                 250                 255
221 Thr Val Phe Arg Pro Val Ser Glu Thr Cys Thr Asp Arg Ser Gly Ser
222         260                 265                 270
223 Ser Thr Gly His Trp Ser Gly Glu Val Lys Asp Lys Asn Val Gln Val
224         275                 280                 285
225 Val Glu Leu Pro Ile Val Asp Ser Val His Pro Arg Pro Pro Tyr Leu
226         290                 295                 300
227 Pro Leu Ala Val Pro Glu Asp Leu Ala Asp Arg Leu Val Arg Val His
228 305                 310                 315                 320
229 Gly Asp Pro Ala Val Trp Trp Val Ser Gln Phe Val Lys Tyr Leu Ile
230             325                 330                 335
231 Arg Pro Gln Pro Trp Leu Glu Lys Glu Ile Glu Glu Ala Thr Lys Lys
232         340                 345                 350
233 Leu Gly Phe Lys His Pro Val Ile Gly Val His Val Arg Arg Thr Asp
234         355                 360                 365
235 Lys Val Gly Ala Glu Ala Ala Phe His Pro Ile Glu Glu Tyr Thr Val
236     370                 375                 380
237 His Val Glu Glu Asp Phe Gln Leu Leu Ala Arg Arg Met Gln Val Asp
238 385                 390                 395                 400
239 Lys Lys Arg Val Tyr Leu Ala Thr Asp Asp Pro Ala Leu Leu Lys Glu
240             405                 410                 415
241 Ala Lys Thr Lys Tyr Pro Ser Tyr Glu Phe Ile Ser Asp Asn Ser Ile
242             420                 425                 430
243 Ser Trp Ser Ala Gly Leu His Asn Arg Tyr Thr Glu Asn Ser Leu Arg
244         435                 440                 445
245 Gly Val Ile Leu Asp Ile His Phe Leu Ser Gln Ala Asp Phe Leu Val
246     450                 455                 460
247 Cys Thr Phe Ser Ser Gln Val Cys Arg Val Ala Tyr Glu Ile Met Gln
248 465                 470                 475                 480
```

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```
249 Ala Leu His Pro Asp Ala Ser Ala Asn Phe Arg Ser Leu Asp Asp Ile
250              485             490             495
251 Tyr Tyr Phe Gly Gly Pro Asn Ala His Asn Gln Ile Ala Ile Tyr Pro
252              500             505             510
253 His Gln Pro Arg Thr Glu Gly Glu Ile Pro Met Glu Pro Gly Asp Ile
254         515             520             525
255 Ile Gly Val Ala Gly Asn His Trp Asp Gly Tyr Pro Lys Gly Val Asn
256     530             535             540
257 Arg Lys Leu Gly Arg Thr Gly Leu Tyr Pro Ser Tyr Lys Val Arg Glu
258 545             550             555                 560
259 Lys Ile Glu Thr Val Lys Tyr Pro Thr Tyr Pro Glu Ala Asp Lys
260              565             570             575
263 <210> SEQ ID NO: 3
264 <211> LENGTH: 26
265 <212> TYPE: PRT
266 <213> ORGANISM: Artificial Sequence
268 <220> FEATURE:
269 <223> OTHER INFORMATION: Primer
271 <400> SEQUENCE: 3
272 Lys Gln Thr Lys Asn Gly Pro Gly Lys Asp His Glu Ile Leu Arg Arg
273 1               5               10              15
274 Arg Ile Glu Asn Gly Ala Lys Glu Leu Gln
275             20              25
278 <210> SEQ ID NO: 4
279 <211> LENGTH: 10
280 <212> TYPE: PRT
281 <213> ORGANISM: Artificial Sequence
283 <220> FEATURE:
284 <223> OTHER INFORMATION: Primer
286 <400> SEQUENCE: 4
287 Lys Tyr Pro Thr Tyr Pro Glu Ala Asp Lys
288 1               5               10
291 <210> SEQ ID NO: 5
292 <211> LENGTH: 12
293 <212> TYPE: PRT
294 <213> ORGANISM: Artificial Sequence
296 <220> FEATURE:
297 <223> OTHER INFORMATION: Primer
299 <400> SEQUENCE: 5
300 Lys Tyr Leu Ile Arg Pro Gln Pro Trp Leu Glu Lys
301 1               5               10
304 <210> SEQ ID NO: 6
305 <211> LENGTH: 14
306 <212> TYPE: PRT
307 <213> ORGANISM: Artificial Sequence
309 <220> FEATURE:
310 <223> OTHER INFORMATION: Primer
312 <400> SEQUENCE: 6
313 Lys Arg Val Tyr Leu Ala Thr Asp Asp Pro Ala Leu Leu Lys
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VERIFICATION SUMMARY
PATENT APPLICATION: US/09/839,136

DATE: 11/08/2001
TIME: 12:15:50

Input Set : **A:\2356-7 Sequence Listing.txt**
Output Set: **N:\CRF3\11082001\I839136.raw**

L:334 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:353 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8